



IFWO

RAW SEQUENCE LISTING

DATE: 08/09/2004

PATENT APPLICATION: US/10/803,344B

TIME: 11:01:59

Input Set : A:\SYR-HDAC-5005-U sub seq list 2.ST25.txt

Output Set: N:\CRF4\08092004\J803344B.raw

3 <110> APPLICANT: Syrrx, Inc.
 5 <120> TITLE OF INVENTION: HISTONE DEACETYLASE INHIBITORS
 7 <130> FILE REFERENCE: SYR-HDAC-5005-U
 9 <140> CURRENT APPLICATION NUMBER: US 10/803,344B
 10 <141> CURRENT FILING DATE: 2004-03-17
 12 <150> PRIOR APPLICATION NUMBER: US 60/455,437
 13 <151> PRIOR FILING DATE: 2003-03-17
 15 <150> PRIOR APPLICATION NUMBER: US 60/531,203
 16 <151> PRIOR FILING DATE: 2003-12-19
 18 <160> NUMBER OF SEQ ID NOS: 8
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 513
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Artificial
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Residues 1-482 of HDAC1 with a

ENTERED

"MSYYHHHHHHHDYDIPTTENLYFQGAMEPGGS"

29 tag at the N-terminus
 31 <400> SEQUENCE: 1
 33 Met Ser Tyr Tyr His His His His His His Asp Tyr Asp Ile Pro Thr
 34 1 5 10 15
 37 Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Glu Pro Gly Gly Ser Met
 38 20 25 30
 41 Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Asp Gly
 42 35 40 45
 45 Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His
 46 50 55 60
 49 Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr Arg
 50 65 70 75 80
 53 Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met Thr
 54 85 90 95
 57 Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg Pro
 58 100 105 110
 61 Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val Gly
 62 115 120 125
 65 Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu Ser
 66 130 135 140
 69 Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln Thr
 70 145 150 155 160
 73 Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys Ser
 74 165 170 175
 77 Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile Leu
 78 180 185 190

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```

81 Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp Ile
82      195      200      205
85 His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val
86      210      215      220
89 Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr Gly
90 225      230      235      240
93 Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val Asn
94      245      250      255
97 Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
98      260      265      270
101 Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val
102      275      280      285
105 Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
106      290      295      300
109 Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
110 305      310      315      320
113 Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr Ile
114      325      330      335
117 Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
118      340      345      350
121 Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
122      355      360      365
125 Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln
126      370      375      380
129 Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn
130 385      390      395      400
133 Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro
134      405      410      415
137 Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp Pro
138      420      425      430
141 Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
142      435      440      445
145 Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys Asn
146      450      455      460
149 Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys
150 465      470      475      480
153 Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr
154      485      490      495
157 Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys Leu
158      500      505      510

```

161 Ala

165 <210> SEQ ID NO: 2

166 <211> LENGTH: 1542

167 <212> TYPE: DNA

168 <213> ORGANISM: Artificial

170 <220> FEATURE:

171 <223> OTHER INFORMATION: DNA sequence encoding residues 1-482 of HDAC1

with a

172 "MSYYHHHHHHHDYDIPTTENLYFQGAMEPGGS" tag at the N-terminus

174 <400> SEQUENCE: 2

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175 atgtcgtact accatcacca tcaccatcac gattacgata tcccaacgac cgaaaacctg      60
177 tattttcagg gcgccatgga acccggggga tccatggcgc agacgcaggg caccggagg      120
179 aaagtctgtt actactacga cggggatgtt ggaaattact attatggaca aggccaccca      180
181 atgaagcctc accgaatccg catgactcat aatttgctgc tcaactatgg tctctaccga      240
183 aaaatggaaa tctatcgccc tcacaaagcc aatgctgagg agatgaccaa gtaccacagc      300
185 gatgactaca ttaaattctt gcgctccatc cgtccagata acatgtcgga gtacagcaag      360
187 cagatgcaga gattcaacgt tggtagggac tgtccagtat tcgatggcct gtttgagttc      420
189 tgtcagttgt ctactggtgg ttctgtggca agtgtgtgta aacttaataa gcagcagacg      480
191 gacatcgctg tgaattgggc tgggggcctg caccatgcaa agaagtccga ggcctctggc      540
193 ttctgttacg tcaatgatat cgtcttggcc atcctggaac tgctaaagta tcaccagagg      600
195 gtgctgtaca ttgacattga tattcaccat ggtgacggcg tggagaggc cttctacacc      660
197 acggaccggg tcatgactgt gtcccttcat aagtatggag agtacttccc aggaactggg      720
199 gacctacggg atatcggggc tggcaaaggc aagtattatg ctgttaacta cccgctccga      780
201 gacgggattg atgacgagtc ctatgaggcc attttcaagc cggtcatgtc caaagtaatg      840
203 gagatgttcc agcctagtgc ggtggtctta cagtgtggct cagactccct atctggggat      900
205 cggtaggtt gcttcaatct aactatcaaa ggacacgcca agtgtgtgga atttgtcaag      960
207 agctttaacc tgccatgct gatgctggga ggcggtggtt acaccattcg taacgttgcc      1020
209 cggtagtgga catatgagac agctgtggcc ctggatacgg agatccctaa tgagcttcca      1080
211 tacaatgact actttgaata ctttggacca gatttcaagc tccacatcag tccttccaat      1140
213 atgactaacc agaacacgaa tgagtacctg gagaagatca aacagcgact gtttgagaac      1200
215 cttagaatgc tgccgcacgc acctgggggc caaatgcagg cgattcctga ggacgccatc      1260
217 cctgaggaga gtggcgatga ggacgaagac gacctgaca agcgcatctc gatctgctcc      1320
219 tctgacaaac gaattgcctg tgaggaagag ttctccgatt ctgaagagga gggagagggg      1380
221 ggccgcaaga actcttccaa cttcaaaaaa gccaaagagag tcaaaacaga ggatgaaaaa      1440
223 gagaaagacc cagaggagaa gaaagaagtc accgaagagg agaaaaccaa ggaggagaag      1500
225 ccagaagcca aaggggtcaa ggaggaggtc aagttggcct ga      1542

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228 <210> SEQ ID NO: 3

229 <211> LENGTH: 498

230 <212> TYPE: PRT

231 <213> ORGANISM: Artificial

233 <220> FEATURE:

234 <223> OTHER INFORMATION: Residues 1-488 of HDAC2 with a "GHHHHHH" tag at the C-terminus

235 and a "MGS" tag at the N-terminus

237 <400> SEQUENCE: 3

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239 Met Gly Ser Met Ala Tyr Ser Gln Gly Gly Gly Lys Lys Lys Val Cys
240 1          5          10          15
243 Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His
244          20          25          30
247 Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn
248          35          40          45
251 Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr
252          50          55          60
255 Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu
256 65          70          75          80
259 Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln
260          85          90          95
263 Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu
264          100         105         110
267 Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu

```

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```

268          115          120          125
271 Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
272          130          135          140
275 His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
276 145          150          155          160
279 Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
280          165          170          175
283 Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr
284          180          185          190
287 Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr
288          195          200          205
291 Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys
292          210          215          220
295 Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu Ser
296 225          230          235          240
299 Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr
300          245          250          255
303 Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly
304          260          265          270
307 Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys
308          275          280          285
311 Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly
312          290          295          300
315 Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr
316 305          310          315          320
319 Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp
320          325          330          335
323 Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser
324          340          345          350
327 Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln
328          355          360          365
331 Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln
332          370          375          380
335 Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu
336 385          390          395          400
339 Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys
340          405          410          415
343 Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu
344          420          425          430
347 Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys Ala
348          435          440          445
351 Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val
352          450          455          460
355 Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr
356 465          470          475          480
359 Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro Gly His His His His
360          485          490          495
363 His His
367 <210> SEQ ID NO: 4

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Input Set : A:\SYR-HDAC-5005-U sub seq list 2.ST25.txt

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368 <211> LENGTH: 1497

369 <212> TYPE: DNA

370 <213> ORGANISM: Artificial

372 <220> FEATURE:

373 <223> OTHER INFORMATION: DNA sequence encoding residues 1-488 of HDAC2

with a "GHHHHHH"

374 tag at the C-terminus and a "MGS" tag at the N-terminus

376 <400> SEQUENCE: 4

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377 atgggatcca tggcgtagac tcaaggaggc ggcaaaaaaa aagtctgcta ctactacgac      60
379 ggtgatattg gaaattatta ttatggacag ggcatcccca tgaagcctca tagaatccgc      120
381 atgaccataa acttgctgtt aaattatggc ttatacagaa aaatggaaat atataggccc      180
383 cataaagcca ctgccgaaga aatgacaaaa tatcacagtg atgagtatat caaatttcta      240
385 cggatcaataa gaccagataa catgtctgag tatagtaagc agatgcagag atttaattgtt      300
387 ggagaagatt gtccagtgtt tgatggactc tttgagtttt gtcagctctc aactggcggt      360
389 tcagttgctg gagctgtgaa gttaaaccga caacagactg atatggctgt taattgggct      420
391 ggaggattac atcatgctaa gaaatcagaa gcatcaggat tctgttacgt taatgatatt      480
393 gtgcttgcca tccttgaatt actaaagtat catcagagag tcttatatat tgatatagat      540
395 attcatcatg gtgatgggtg tgaagaagct tttatacaaa cagatcgtgt aatgacggta      600
397 tcattccata aatatgggga atactttcct ggcacaggag acttgaggga tattggtgct      660
399 ggaaaaggca aatactatgc tgtcaatttt ccaatgagag atggtataga tgatgagtca      720
401 tatgggcaga tatttaagcc tattatctca aaggtgatgg agatgtatca acctagtgtc      780
403 gtggtattac agtgtggtgc agactcatta tctggtgata gactgggttg tttcaatcta      840
405 acagtcaaag gtcatgctaa atgtgtagaa gttgtaaaaa cttttaactt accattactg      900
407 atgcttggag gaggtggcta cacaatccgt aatgttgctc gatgttgga atatgagact      960
409 gcagttgccc ttgattgtga gattcccaat gagttgccat ataatgatta ctttgagtat     1020
411 tttggaccag acttcaaact gcatattagt cttcaaaca tgacaaacca gaacactcca     1080
413 gaatatatgg aaaagataaa acagcgtttg tttgaaaatt tgccgatgtt acctcatgca     1140
415 cctggtgtcc agatgcaagc tattccagaa gatgctgttc atgaagacag tggagatgaa     1200
417 gatggagaag atccagacaa gagaatttct attcgagcat cagacaagcg gatagcttgt     1260
419 gatgaagaat tctcagattc tgaggatgaa ggagaaggag gtcgaagaaa tgtggctgat     1320
421 cataagaaag gagcaaagaa agctagaatt gaagaagata agaaagaaac agaggacaaa     1380
423 aaaacagacg ttaaggaaga agataaatcc aaggacaaca gtggtgaaaa aacagatacc     1440
425 aaaggaacca aatcagaaca gctcagcaac cccgggcatc accatcacca tcactaa      1497

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428 <210> SEQ ID NO: 5

429 <211> LENGTH: 782

430 <212> TYPE: PRT

431 <213> ORGANISM: Artificial

433 <220> FEATURE:

434 <223> OTHER INFORMATION: Residues 73-845 of HDAC6 with a "GHHHHHH" tag at the C-terminus

435 and a "MP" tag at the N-terminus

437 <400> SEQUENCE: 5

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439 Met Pro Gly Met Asp Leu Asn Leu Glu Ala Glu Ala Leu Ala Gly Thr
440 1          5          10          15
443 Gly Leu Val Leu Asp Glu Gln Leu Asn Glu Phe His Cys Leu Trp Asp
444          20          25          30
447 Asp Ser Phe Pro Glu Gly Pro Glu Arg Leu His Ala Ile Lys Glu Gln
448          35          40          45
451 Leu Ile Gln Glu Gly Leu Leu Asp Arg Cys Val Ser Phe Gln Ala Arg
452          50          55          60
455 Phe Ala Glu Lys Glu Glu Leu Met Leu Val His Ser Leu Glu Tyr Ile

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8

VERIFICATION SUMMARY

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